



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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- (ii) TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
- (iii) NUMBER OF SEQUENCES: 356
- (iv) CORRESPONDENCE ADDRESS:
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- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1
- (vi) CURRENT APPLICATION DATA:
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(A) APPLICATION NUMBER: 08/465,380

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGGCATACC CGGAGTGTGG TGAGAATGAA TGGCTCGACG ACTGTGGAAC TCAGAACCCA	60
TGCGAGGCCA AGTCAATGA GGAACCCCT GAGGAGGAAG ATCCGATATG CCGCTCACGT	120
GGTTGTTTAT TACCTCCTGC TTGCGTATGC AAAGACGGAT TCTACAGAGA CACGGTGATC	180
GGCGACTGTG TTAGGAAAGA AGAATGCGAC CAACATGAGA TTATACATGT CTGA	234

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGCATACC CGGAGTGTGG TGAGAATGAA TGGCTCGACG TCTGTGGAAC TAAGAACCCA	60
TGCGAGGCCA AGTCAGTGA GGAAGAGGAG GAAGATCCGA TATGCCGATC ATTTCTTGT	120
CCGGGTCCCG CTGCTTGCCT ATGCGAAGAC GGATTCTACA GAGACACGGT GATCGGCAC	180
TGTGTTAAGG AAGAAGATG CGACCAACAT GAGATTATAAC ATGTCTGA	228

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ancylostoma caninum*

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCGCT ACTACTCAAC A	ATG AAG ATG CTT TAC GCT ATC GCT ATA ATG	51
	Met Lys Met Leu Tyr Ala Ile Ala Ile Met	
1	5	10
TTT CTC CTG GTA TCA TTA TGC AGC GCA AGA ACA GTG AGG AAG GCA TAC		99
Phe Leu Leu Val Ser Leu Cys Ser Ala Arg Thr Val Arg Lys Ala Tyr		
15	20	25
CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC GAC TGT GGA ACT CAG AAG		147
Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp Cys Gly Thr Gln Lys		
30	35	40
CCA TGC GAG GCC AAG TGC AAT GAG GAA CCC CCT GAG GAG GAA GAT CCG		195
Pro Cys Glu Ala Lys Cys Asn Glu Glu Pro Pro Glu Glu Glu Asp Pro		
45	50	55
ATA TGC CGC TCA CGT GGT TGT TTA TTA CCT CCT GCT TGC GTA TGC AAA		243
Ile Cys Arg Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys Val Cys Lys		
60	65	70
GAC GGA TTC TAC AGA GAC ACG GTG ATC GGC GAC TGT GTT AGG GAA GAA		291
Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu		
75	80	85
90		
GAA TGC GAC CAA CAT GAG ATT ATA CAT GTC T GAACGAGAAA GCAACAATAA CC		344
Glu Cys Asp Gln His Glu Ile Ile His Val		
95	100	
AAAGGTTCCA ACTCTCGCTC TGCAAAATCG CTAGTTGGAT GTCTCTTTG CGTCCGAATA		404
GTTTTAGTTG ATGTTAAGTA AGAACTCCTG CTGGAGAGAA TAAAGCTTTC CAACTCC		461

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys	Ala	Tyr	Pro	Glu	Cys	Gly	Glu	Asn	Glu	Trp	Leu	Asp	Asp
1				5					10				
Cys	Gly	Thr	Gln	Lys	Pro	Cys	Glu	Ala	Lys	Cys	Asn	Glu	Glu
15				20					25				
Pro	Pro	Glu	Glu	Asp	Pro	Ile	Cys	Arg	Ser	Arg	Gly	Cys	
30		35						40					
Leu	Leu	Pro	Pro	Ala	Cys	Val	Cys	Lys	Asp	Gly	Phe	Tyr	Arg
45					50						55		
Asp	Thr	Val	Ile	Gly	Asp	Cys	Val	Arg	Glu	Glu	Cys	Asp	
60					65						70		
Gln	His	Glu	Ile	Ile	His	Val							
					75								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	455 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

(A) NAME/KEY:	Coding Sequence
(B) LOCATION:	22...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCT ACTACTAAC A ATG AAG ATG CTT TAC GCT ATC GCT ATA ATG	51
Met Lys Met Leu Tyr Ala Ile Ala Ile Met	
1 5 10	
TTT CTC CTG GTG TCA TTA TGC AGC ACA AGA ACA GTG AGG AAG GCA TAC	99
Phe Leu Leu Val Ser Leu Cys Ser Thr Arg Thr Val Arg Lys Ala Tyr	
15 20 25	
CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC GTC TGT GGA ACT AAG AAG	147
Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Val Cys Gly Thr Lys Lys	
30 35 40	
CCA TGC GAG GCC AAG TGC AGT GAG GAA GAG GAG GAA GAT CCG ATA TGC	195
Pro Cys Glu Ala Lys Cys Ser Glu Glu Glu Glu Asp Pro Ile Cys	
45 50 55	
CGA TCA TTT TCT TGT CCG GGT CCC GCT GCT TGC GTA TGC GAA GAC GGA	243
Arg Ser Phe Ser Cys Pro Gly Pro Ala Ala Cys Val Cys Glu Asp Gly	
60 65 70	

TTC TAC AGA GAC ACG GTG ATC GGC GAC TGT GTT AAG GAA GAA GAA TGC Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys 75 80 85 90	291
GAC CAA CAT GAG ATT ATT CAT GTC TGAACGAGAG AGCAGTAATA ACCAAAGGTT C Asp Gln His Glu Ile Ile His Val 95	346
CAACTTCGC TCTACAAAAT CGCTAGTTGG ATTTCTCCTT TGCGTGCGAA TAGTTTAGT TGATATTAAG TAAAACCTCC TGTTGAAGAG AATAAGCTT TCCAACCTTC	406 455

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Val Cys Gly 1 5 10 15
Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu Glu Glu Asp 20 25 30
Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly Pro Ala Ala Cys Val Cys 35 40 45
Glu Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu 50 55 60
Glu Glu Cys Asp Gln His Glu Ile Ile His Val 65 70 75

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu 1 5 10 15
Asp Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu Glu 20 25 30

Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly Cys Leu Leu
 35 40 45

Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg Asp Thr Val Ile
 50 55 60

Gly Asp Cys Val Arg Glu Glu Cys Asp Gln His Glu Ile Ile His
 65 70 75 80

Val

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu
 1 5 10 15

Asp Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu
 20 25 30

Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly Pro Ala
 35 40 45

Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp
 50 55 60

Cys Val Lys Glu Glu Cys Asp Gln His Glu Ile Ile His Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma ceylanicum

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 21...590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCACTA TTATCCAACA	ATG GCG GTG CTT TAT TCA GTA GCA ATA GCG	50
	Met Ala Val Leu Tyr Ser Val Ala Ile Ala	
	1 5 10	
TTA CTA CTG GTA TCA CAA TGC AGT GGG AAA CCG AAC AAT GTG ATG ACT		98
Leu Leu Leu Val Ser Gln Cys Ser Gly Lys Pro Asn Asn Val Met Thr		
15 20 25		
AAC GCT TGT GGT CTT AAT GAA TAT TTC GCT GAG TGT GGC AAT ATG AAG		146
Asn Ala Cys Gly Leu Asn Glu Tyr Phe Ala Glu Cys Gly Asn Met Lys		
30 35 40		
GAA TGC GAG CAC AGA TGC AAT GAG GAG GAA AAT GAG GAA AGG GAC GAG		194
Glu Cys Glu His Arg Cys Asn Glu Glu Asn Glu Glu Arg Asp Glu		
45 50 55		
GAA AGA ATA ACG GCA TGC CTC ATC CGT GTG TGT TTC CGT CCT GGT GCT		242
Glu Arg Ile Thr Ala Cys Leu Ile Arg Val Cys Phe Arg Pro Gly Ala		
60 65 70		
TGC GTA TGC AAA GAC GGA TTC TAT AGA AAC AGA ACA GGC AGC TGT GTG		290
Cys Val Cys Lys Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser Cys Val		
75 80 85 90		
GAA GAA GAT GAC TGC GAG TAC GAG AAT ATG GAG TTC ATT ACT TTT GCA		338
Glu Glu Asp Asp Cys Glu Tyr Glu Asn Met Glu Phe Ile Thr Phe Ala		
95 100 105		
CCA GAA GTA CCG ATA TGT GGT TCC AAC GAA AGG TAC TCC GAC TGC GGC		386
Pro Glu Val Pro Ile Cys Gly Ser Asn Glu Arg Tyr Ser Asp Cys Gly		
110 115 120		
AAT GAC AAA CAA TGC GAG CGC AAA TGC AAC GAG GAC GAT TAT GAG AAG		434
Asn Asp Lys Gln Cys Glu Arg Lys Cys Asn Glu Asp Asp Tyr Glu Lys		
125 130 135		
GGA GAT GAG GCA TGC CGC TCA CAT GTT TGT GAA CGT CCT GGT GCC TGT		482
Gly Asp Glu Ala Cys Arg Ser His Val Cys Glu Arg Pro Gly Ala Cys		
140 145 150		
GTA TGC GAA GAC GGG TTC TAC AGA AAC AAA AAA GGT AGC TGT GTG GAA		530
Val Cys Glu Asp Gly Phe Tyr Arg Asn Lys Lys Gly Ser Cys Val Glu		
155 160 165 170		
AGC GAT GAC TGC GAA TAC GAT AAT ATG GAT TTC ATC ACT TTT GCA CCA		578
Ser Asp Asp Cys Glu Tyr Asp Asn Met Asp Phe Ile Thr Phe Ala Pro		
175 180 185		
GAA ACC TCA CGA TAACCAAAGA TGCTACCTCT CGTACGCAAC TCCGCTGATT GAGGTT		636
Glu Thr Ser Arg		
190		
GATTCACTCC CTTGCATCTC AACATTTTT TTGTGATGCT GTGCATCTGA GCTTAACCTG		696
ATAAAGCCTA TGGTG		711

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma ceylanicum

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 10...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCCGC ATG CGG ACG CTC TAC CTC ATT TCT ATC TGG TTG TTC CTC ATC Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu Phe Leu Ile	51
1 5 10	
TCG CAA TGT AAT GGA AAA GCA TTC CCG AAA TGT GAC GTC AAT GAA AGA Ser Gln Cys Asn Gly Lys Ala Phe Pro Lys Cys Asp Val Asn Glu Arg	99
15 20 25 30	
TTC GAG GTG TGT GGC AAT CTG AAG GAG TGC GAG CTC AAG TGC GAT GAG Phe Glu Val Cys Gly Asn Leu Lys Glu Cys Glu Leu Lys Cys Asp Glu	147
35 40 45	
GAC CCT AAG ATA TGC TCT CGT GCA TGT ATT CGT CCC CCT GCT TGC GTA Asp Pro Lys Ile Cys Ser Arg Ala Cys Ile Arg Pro Pro Ala Cys Val	195
50 55 60	
TGC GAT GAC GGA TTC TAC AGA GAC AAA TAT GGC TTC TGT GTT GAA GAA Cys Asp Gly Phe Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu	243
65 70 75	
GAC GAA TGT AAC GAT ATG GAG ATT ATT ACT TTT CCA CCA GAA ACC AAA TG Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys	293
80 85 90	
ATGACCGAAG CTTCCACCTT TCTATACATA TCTTCACTGC TTGACAGGCT TCTCGACAAT	353
TTAGAAGTTC TGCTTGACTT TGTCTATTG AAATTGTTCA CACTAATGGG GGAAGTAAAG	413
CATTTCACG AC	425

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma ceylanicum

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 23...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCCGCT ACATTTCAA CA ATG TCG ACG CTT TAT GTT ATC GCA ATA TGT	52
Met Ser Thr Leu Tyr Val Ile Ala Ile Cys	
1 5 10	
TTG CTG CTT GTT TCG CAA TGC AAT GGA AGA ACG GTG AAG AAG TGT GGC	100
Leu Leu Leu Val Ser Gln Cys Asn Gly Arg Thr Val Lys Lys Cys Gly	
15 20 25	
AAG AAT GAA AGA TAC GAC GAC TGT GGC AAT GCA AAG GAC TGC GAG ACC	148
Lys Asn Glu Arg Tyr Asp Asp Cys Gly Asn Ala Lys Asp Cys Glu Thr	
30 35 40	
AAG TGC GGT GAA GAG GAA AAG GTG TGC CGT TCG CGT GAG TGT ACT AGT	196
Lys Cys Gly Glu Glu Lys Val Cys Arg Ser Arg Glu Cys Thr Ser	
45 50 55	
CCT GGT GCC TGC GTA TGC GAA CAA GGA TTC TAC AGA GAT CCG GCT GGC	244
Pro Gly Ala Cys Val Cys Glu Gln Gly Phe Tyr Arg Asp Pro Ala Gly	
60 65 70	
GAC TGT GTC ACT GAT GAA GAA TGT GAT GAA TGG AAC AAT ATG GAG ATC	292
Asp Cys Val Thr Asp Glu Cys Asp Glu Trp Asn Asn Met Glu Ile	
75 80 85 90	
ATT ACT ATG CCA AAA CAG TAGTGCAG TTCCCTTCTT TCTCAAATC TGCTCCGTG	349
Ile Thr Met Pro Lys Gln	
95	
CTCAATTATC ACACACCTCC ACTAGTTAAG ATTGACTGAC TCTCTTGCAT TGTAGTATT	409
TCGCTTGACT CTGTGCATTT AAGCATGAGA TACTACTAGG GAGAATAAAA ATTACTAACT	469
AC	471

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma duodenale

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 10...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCCGG AAA TGT CCT ACC GAT GAA TGG TTC GAT TGG TGT GGA ACT TAC	51
Lys Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr	
1 5 10	
AAG CAT TGC GAA CTC AAG TGC GAT AGG GAG CTA ACT GAG AAA GAA GAG	99

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 21...560

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ancylostoma duodenale*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCCGGG CGGCAGAAAG	ATG CGA ATG CTC TAC CTT GTT CCT ATC TGG	50
	Met Arg Met Leu Tyr Leu Val Pro Ile Trp	
	1 5 10	
TTG CTG CTC ATT TCG CTA TGC AGT GGA AAA GCT GCG AAG AAA TGT GGT	98	
Leu Leu Leu Ile Ser Leu Cys Ser Gly Lys Ala Ala Lys Lys Cys Gly		
15 20 25		
CTC AAT GAA AGG CTG GAC TGT GGC AAT CTG AAG CAA TGC GAG CCC AAG	146	
Leu Asn Glu Arg Leu Asp Cys Gly Asn Leu Lys Gln Cys Glu Pro Lys		
30 35 40		
TGC AGC GAC TTG GAA AGT GAG GAG TAT GAG GAG GAA GAT GAG TCG AAA	194	
Cys Ser Asp Leu Glu Ser Glu Glu Tyr Glu Glu Asp Glu Ser Lys		
45 50 55		
TGT CGA TCA CGT GAA TGT TCT CGT CGT GTT TGT GTA TGC GAT GAA GGA	242	
Cys Arg Ser Arg Glu Cys Ser Arg Arg Val Cys Val Cys Asp Glu Gly		
60 65 70		

TTC TAC AGA AAC AAG AAG GGC AAG TGT GTT GCA AAA GAT GTT TGC GAG Phe Tyr Arg Asn Lys Lys Gly Lys Cys Val Ala Lys Asp Val Cys Glu 75 80 85 90	290
GAC GAC AAT ATG GAG ATT ATC ACT TTT CCA CCA GAA GAC GAA TGT GGT Asp Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Glu Cys Gly 95 100 105	338
CCC GAT GAA TGG TTC GAC TAC TGT GGA AAT TAT AAG AAG TGC GAA CGC Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys Lys Cys Glu Arg 110 115 120	386
AAG TGC AGT GAG GAG ACA AGT GAG AAA AAT GAG GAG GCA TGC CTC TCT Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Ala Cys Leu Ser 125 130 135	434
CGT GCT TGT ACT GGT CGT GCT TGC GTA TGC AAA GAC GGA TTG TAC AGA Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Lys Asp Gly Leu Tyr Arg 140 145 150	482
GAC GAC TTT GGC AAC TGT GTT CCA CAT GAC GAA TGC AAC GAT ATG GAG Asp Asp Phe Gly Asn Cys Val Pro His Asp Glu Cys Asn Asp Met Glu 155 160 165 170	530
ATC ATC ACT TTT CCA CCG GAA ACC AAA CAT TGACCAGAGG CTCCAACCTCT CGCT Ile Ile Thr Phe Pro Pro Glu Thr Lys His 175 180	584
ACACAAACGTC AGGGCTAGAA TGGCCCTCT GCGAGTTAGT AGTTTGCTT GACTCTGCTT ATTTGAGCAC TTTCTATTGA TGGCGAAAAT AAAGCATTAA AAAC	644
	688

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Heligmosomoides polygyrus*

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCCGCG CACCTGAGAG GTGAGCTACG CAAGTCTTCG CTGGTACA ATG ATC CGA Met Ile Arg 1	57
AAG CTC GTT CTG CTG ACT GCT ATC GTC ACG GTG GTG CTA AGT GCG AAG Lys Leu Val Leu Leu Thr Ala Ile Val Thr Val Val Leu Ser Ala Lys 5 10 15	105

ACC TGT GGA CCA AAC GAG GAG TAC ACT GAA TGC GGG ACG CCA TGC GAG Thr Cys Gly Pro Asn Glu Glu Tyr Thr Glu Cys Gly Thr Pro Cys Glu 20 25 30 35	153
CCG AAG TGC AAT GAA CCG ATG CCA GAC ATC TGT ACT CTG AAC TGC ATC Pro Lys Cys Asn Glu Pro Met Pro Asp Ile Cys Thr Leu Asn Cys Ile 40 45 50	201
GTG AAC GTG TGT CAG TGC AAA CCC GGC TTC AAG CGC GGA CCG AAA GGA Val Asn Val Cys Gln Cys Lys Pro Gly Phe Lys Arg Gly Pro Lys Gly 55 60 65	249
TGC GTC GCC CCC GGA CCA GGC TGT AAA TAGTTCTCCA CCTGCCCTTT CGTTGGAA Cys Val Ala Pro Gly Pro Gly Cys Lys 70 75	304
CAAATGGCTG TCTTTTACA TTCTGAATCA ATAAAGCCGA ACGGT	349

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT CTT TTG Met Pro Val Leu Leu 1 5	54
GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT CTG GTA ACT TTG Gly Ile Pro Leu Leu Arg Phe Leu Gly Phe Leu Leu Val Thr Leu 10 15 20	102
TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG GGC TTC GGT AAG ATA GCT Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys Gly Phe Gly Lys Ile Ala 25 30 35	150
ATT GCT ATT TCA TTG TTT CTT GCT CTT ATT ATT GGG CTT AAC TCA ATT Ile Ala Ile Ser Leu Phe Leu Ala Leu Ile Ile Gly Leu Asn Ser Ile 40 45 50	198
CTT GTG GGT TAT CTC TCT GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT Leu Val Gly Tyr Leu Ser Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe 55 60 65	246
GTT CAG GGC GTT CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT Val Gln Gly Val Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe 70 75 80 85	294
TAT GTT ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA Tyr Val Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys 90 95 100	342

CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC TCA GGC Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly Ser Gly 105 110 115	390
GGA GGCCAAGTCG GCCATCCCAT ATCACGCGGC CGCGGATCC Gly	432

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAGCTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT CTT TTG Met Pro Val Leu Leu 1 5	54
GGT ATT CCG TTA TTG CGT TTC CTC GGT TTC CTT CTG GTA ACT TTG Gly Ile Pro Leu Leu Arg Phe Leu Gly Phe Leu Leu Val Thr Leu 10 15 20	102
TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG GGC TTC GGT AAG ATA GCT Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys Gly Phe Gly Lys Ile Ala 25 30 35	150
ATT GCT ATT TCA TTG TTT CTT GCT CTT ATT ATT GGG CTT AAC TCA ATT Ile Ala Ile Ser Leu Phe Leu Ala Leu Ile Ile Gly Leu Asn Ser Ile 40 45 50	198
CTT GTG GGT TAT CTC TCT GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT Leu Val Gly Tyr Leu Ser Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe 55 60 65	246
GTT CAG GGC GTT CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT Val Gln Gly Val Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe 70 75 80 85	294
TAT GTT ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA Tyr Val Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys 90 95 100	342
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC TCA GGC Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Ser Gly 105 110 115	390
GGA GGGCCAAGTC GGCCATCCCA TATCACGCGG CGCGGATCC Gly	433

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGCTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT CTT TTG Met Pro Val Leu Leu	54
1 5	
GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT CTG GTA ACT TTG Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu Leu Val Thr Leu	102
10 15 20	
TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG GGC TTC GGT AAG ATA GCT Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys Gly Phe Gly Lys Ile Ala	150
25 30 35	
ATT GCT ATT TCA TTG TTT CTT GCT CTT ATT ATT GGG CTT AAC TCA ATT Ile Ala Ile Ser Leu Phe Leu Ala Leu Ile Ile Gly Leu Asn Ser Ile	198
40 45 50	
CTT GTG GGT TAT CTC TCT GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT Leu Val Gly Tyr Leu Ser Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe	246
55 60 65	
GTT CAG GGC GTT CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT Val Gln Gly Val Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe	294
70 75 80 85	
TAT GTT ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA Tyr Val Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys	342
90 95 100	
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC TCA GGC Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Ser Gly	390
105 110 115	
GGA TCGGCCAAGT CGGCCATCCC ATATCACGCG GCCGCGGATC C Gly	434

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Gly Gly Ser Gly Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 10...282

(D) OTHER INFORMATION: "W" stands for A or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCCGG CTG GTW TCC TAC TGC AGT GGA AAA GCA ACG ATG CAG TGT GGT	51
Leu Val Ser Tyr Cys Ser Gly Lys Ala Thr Met Gln Cys Gly	
1 5 10	
GAG AAT GAA AAG TAC GAT TCG TGC GGT AGC AAG GAG TGC GAT AAG AAG	99
Glu Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys Glu Cys Asp Lys Lys	
15 20 25 30	
TGC AAA TAT GAC GGA GTT GAG GAG GAA GAC GAC GAG GAA CCT AAT GTG	147
Cys Lys Tyr Asp Gly Val Glu Glu Asp Asp Glu Glu Pro Asn Val	
35 40 45	
CCA TGC CTA GTA CGT GTG TGT CAT CAA GAT TGC GTA TGC GAA GAA GGA	195
Pro Cys Leu Val Arg Val Cys His Gln Asp Cys Val Cys Glu Glu Gly	
50 55 60	
TTC TAT AGA AAC AAA GAT GAC AAA TGT GTA TCA GCA GAA GAC TGC GAA	243
Phe Tyr Arg Asn Lys Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu	
65 70 75	
CTT GAC AAT ATG GAC TTT ATA TAT CCC GGA ACT CGA AAC TGAACGAAGG CTC	295
Leu Asp Asn Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn	
80 85 90	
CATTCTTGCT GCACAAGATC GATTGTCTCT CCCCTGCATC TCAGTAGTT TGCTACATTG	355
TATATGGTAG CAAAAAATTA GCTTAGGGAG AATAAAATCT TTACCTATAT TTAATCAATG	415
AAGTATTCTC TTTCT	430

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Lys	Met	Leu	Tyr	Ala	Ile	Ala	Ile	Met	Phe	Leu	Leu	Val	Ser	Leu
1				5					10					15	
Cys	Ser	Ala	Arg	Thr	Val	Arg	Lys	Ala	Tyr	Pro	Glu	Cys	Gly	Glu	Asn
				20				25				30			
Glu	Trp	Leu	Asp	Asp	Cys	Gly	Thr	Gln	Lys	Pro	Cys	Glu	Ala	Lys	Cys
				35			40				45				
Asn	Glu	Glu	Pro	Pro	Glu	Glu	Asp	Pro	Ile	Cys	Arg	Ser	Arg	Gly	
				50			55		60						
Cys	Leu	Leu	Pro	Pro	Ala	Cys	Val	Cys	Lys	Asp	Gly	Phe	Tyr	Arg	Asp
				65			70		75			80			
Thr	Val	Ile	Gly	Asp	Cys	Val	Arg	Glu	Glu	Glu	Cys	Asp	Gln	His	Glu
				85				90				95			
Ile	Ile	His	Val												
			100												

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Lys	Met	Leu	Tyr	Ala	Ile	Ala	Ile	Met	Phe	Leu	Leu	Val	Ser	Leu
1				5					10					15	
Cys	Ser	Thr	Arg	Thr	Val	Arg	Lys	Ala	Tyr	Pro	Glu	Cys	Gly	Glu	Asn
				20				25				30			
Glu	Trp	Leu	Asp	Val	Cys	Gly	Thr	Lys	Lys	Pro	Cys	Glu	Ala	Lys	Cys
				35			40				45				

Ser Glu Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro
 50 55 60
 Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr Val
 65 70 75 80
 Ile Gly Asp Cys Val Lys Glu Glu Cys Asp Gln His Glu Ile Ile
 85 90 95
 His Val

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu Phe Leu Ile Ser Gln
 1 5 10 15

Cys Asn Gly Lys Ala Phe Pro Lys Cys Asp Val Asn Glu Arg Phe Glu
 20 25 30

Val Cys Gly Asn Leu Lys Glu Cys Glu Leu Lys Cys Asp Glu Asp Pro
 35 40 45
 Lys Ile Cys Ser Arg Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp
 50 55 60

Asp Gly Phe Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu Asp Glu
 65 70 75 80

Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Thr	Leu	Tyr	Val	Ile	Ala	Ile	Cys	Leu	Leu	Leu	Val	Ser	Gln
1				5				10					15		
Cys	Asn	Gly	Arg	Thr	Val	Lys	Lys	Cys	Gly	Lys	Asn	Glu	Arg	Tyr	Asp
				20			25					30			
Asp	Cys	Gly	Asn	Ala	Lys	Asp	Cys	Glu	Thr	Lys	Cys	Gly	Glu	Glu	
				35		40				45					
Lys	Val	Cys	Arg	Ser	Arg	Glu	Cys	Thr	Ser	Pro	Gly	Ala	Cys	Val	Cys
				50		55			60						
Glu	Gln	Gly	Phe	Tyr	Arg	Asp	Pro	Ala	Gly	Asp	Cys	Val	Thr	Asp	Glu
	65			70			75					80			
Glu	Cys	Asp	Glu	Trp	Asn	Asn	Met	Glu	Ile	Ile	Thr	Met	Pro	Lys	Gln
				85			90				95				

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	108 amino acids
(B) TYPE:	amino acid
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ala	Val	Leu	Tyr	Ser	Val	Ala	Ile	Ala	Leu	Leu	Leu	Val	Ser	Gln
1				5				10					15		
Cys	Ser	Gly	Lys	Pro	Asn	Asn	Val	Met	Thr	Asn	Ala	Cys	Gly	Leu	Asn
				20			25				30				
Glu	Tyr	Phe	Ala	Glu	Cys	Gly	Asn	Met	Lys	Glu	Cys	Glu	His	Arg	Cys
				35		40			45						
Asn	Glu	Glu	Glu	Asn	Glu	Glu	Arg	Asp	Glu	Arg	Ile	Thr	Ala	Cys	
				50		55			60						
Leu	Ile	Arg	Val	Cys	Phe	Arg	Pro	Gly	Ala	Cys	Val	Cys	Lys	Asp	Gly
				65		70			75			80			
Phe	Tyr	Arg	Asn	Arg	Thr	Gly	Ser	Cys	Val	Glu	Glu	Asp	Asp	Cys	Glu
				85			90			95					
Tyr	Glu	Asn	Met	Glu	Phe	Ile	Thr	Phe	Ala	Pro	Glu				
				100			105								

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val	Pro	Ile	Cys	Gly	Ser	Asn	Glu	Arg	Tyr	Ser	Asp	Cys	Gly	Asn	Asp
1				5				10						15	

Lys	Gln	Cys	Glu	Arg	Lys	Cys	Asn	Glu	Asp	Asp	Tyr	Glu	Lys	Gly	Asp
				20				25				30			

Glu	Ala	Cys	Arg	Ser	His	Val	Cys	Glu	Arg	Pro	Gly	Ala	Cys	Val	Cys
				35			40				45				

Glu	Asp	Gly	Phe	Tyr	Arg	Asn	Lys	Lys	Gly	Ser	Cys	Val	Glu	Ser	Asp
	50				55					60					

Asp	Cys	Glu	Tyr	Asp	Asn	Met	Asp	Phe	Ile	Thr	Phe	Ala	Pro	Glu	Thr
				65		70			75				80		

Ser Arg

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys	Cys	Pro	Thr	Asp	Glu	Trp	Phe	Asp	Trp	Cys	Gly	Thr	Tyr	Lys	His
1				5				10					15		

Cys	Glu	Leu	Lys	Cys	Asp	Arg	Glu	Leu	Thr	Glu	Glu	Gln	Ala	Cys
			20					25				30		

Leu	Ser	Arg	Val	Cys	Glu	Lys	Ser	Ala	Cys	Val	Cys	Asn	Asp	Gly	Leu
			35			40					45				

Tyr	Arg	Asp	Lys	Phe	Gly	Asn	Cys	Val	Glu	Lys	Asp	Glu	Cys	Asn	Asp
	50				55					60					

Met Glu Ile Ile Thr Phe Ala Pro Glu Thr Lys

65

70

75

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Arg	Met	Leu	Tyr	Leu	Val	Pro	Ile	Trp	Leu	Leu	Leu	Ile	Ser	Leu
1				5				10					15		

Cys	Ser	Gly	Lys	Ala	Ala	Lys	Lys	Cys	Gly	Leu	Asn	Glu	Arg	Leu	Asp
			20				25				30				

Cys	Gly	Asn	Leu	Lys	Gln	Cys	Glu	Pro	Lys	Cys	Ser	Asp	Leu	Glu	Ser
			35			40				45					

Glu	Glu	Tyr	Glu	Glu	Glu	Asp	Glu	Ser	Lys	Cys	Arg	Ser	Arg	Glu	Cys
50				55				60							

Ser	Arg	Arg	Val	Cys	Val	Cys	Asp	Glu	Gly	Phe	Tyr	Arg	Asn	Lys	Lys
65				70				75				80			

Gly	Lys	Cys	Val	Ala	Lys	Asp	Val	Cys	Glu	Asp	Asp	Asn	Met	Glu	Ile
				85			90					95			

Ile	Thr	Phe	Pro	Pro	Glu										
				100											

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp	Glu	Cys	Gly	Pro	Asp	Glu	Trp	Phe	Asp	Tyr	Cys	Gly	Asn	Tyr	Lys
1				5				10				15			

Lys	Cys	Glu	Arg	Lys	Cys	Ser	Glu	Glu	Thr	Ser	Glu	Lys	Asn	Glu	Glu
				20				25				30			
Ala	Cys	Leu	Ser	Arg	Ala	Cys	Thr	Gly	Arg	Ala	Cys	Val	Cys	Lys	Asp
				35				40				45			
Gly	Leu	Tyr	Arg	Asp	Asp	Phe	Gly	Asn	Cys	Val	Pro	His	Asp	Glu	Cys
				50				55			60				
Asn	Asp	Met	Glu	Ile	Ile	Thr	Phe	Pro	Pro	Glu	Thr	Lys	His		
				65				70			75				

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	76 amino acids
(B) TYPE:	amino acid
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM:	Heligmosomoides polygyrus
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Ile	Arg	Lys	Leu	Val	Leu	Leu	Thr	Ala	Ile	Val	Thr	Val	Val	Leu
1				5				10					15		

Ser	Ala	Lys	Thr	Cys	Gly	Pro	Asn	Glu	Glu	Tyr	Thr	Glu	Cys	Gly	Thr
				20				25				30			

Pro	Cys	Glu	Pro	Lys	Cys	Asn	Glu	Pro	Met	Pro	Asp	Ile	Cys	Thr	Leu
				35				40			45				

Asn	Cys	Ile	Val	Asn	Val	Cys	Gln	Cys	Lys	Pro	Gly	Phe	Lys	Arg	Gly
				50				55			60				

Pro	Lys	Gly	Cys	Val	Ala	Pro	Gly	Pro	Gly	Cys	Lys				
				65				70			75				

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	187 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTATTCGAAA	CGATGTTCTC	TCCAATTGG	TCCTTGAA	TTATTTAGC	TACTTGCAA		60
TCTGTCTTCG	CCCAGCCAGT	TATCTCCACT	ACCGTTGGTT	CCGCTGCCGA	GGGTTCTTTG		120

GACAAGAGGC CTATCCGCGG AATTCA GATC TGAATGCGGC CGCTCGAGAC TAGTGGATCC	180
TTAGACA	187

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ancylostoma caninum*

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 36...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCCGCG GAATTCCGCT TGCTACTACT CAACG ATG AAG ACG CTC TAT ATT Met Lys Thr Leu Tyr Ile 1 5	53
GTC GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT GGA AAA CCT TCG Val Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Lys Pro Ser 10 15 20	101
GAG AAA GAA TGT GGT CCC CAT GAA AGA CTC GAC TGT GGC AAC AAG AAG Glu Lys Glu Cys Gly Pro His Glu Arg Leu Asp Cys Gly Asn Lys Lys 25 30 35	149
CCA TGC GAG CGC AAG TGC AAA ATA GAG ACA AGT GAG GAG GAG GAT GAC Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu Glu Glu Asp Asp 40 45 50	197
TAC GAA GAG GGA ACC GAA CGT TTT CGA TGC CTC TTA CGT GTG TGT GAT Tyr Glu Glu Gly Thr Glu Arg Phe Arg Cys Leu Leu Arg Val Cys Asp 55 60 65 70	245
CAG CCT TAT GAA TGC ATA TGC GAT GAT GGA TAC TAC AGA AAC AAG AAA Gln Pro Tyr Glu Cys Ile Cys Asp Asp Gly Tyr Tyr Arg Asn Lys Lys 75 80 85	293
GGC GAA TGT GTG ACT GAT GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu Phe 90 95 100	341
ATT ACT TTC GCA CCA TAAACCCAAT AATGACCAAT GACTCCCATT CTTCGTGATC AG Ile Thr Phe Ala Pro 105	398
CGTCGGTGTT TGACAGTCTC CCCTACATCT TAGTAGTTTT GCTTGATAAT GTATACATAA ACTGTACTTT CTGAGATAGA ATAAAGCTCT CAACTAC	458 495

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ancylostoma caninum*

(ix) FEATURE :

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 24...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCCGCG	GAATTCCGCA	ACG ATG AAG ACG CTC TAT ATT ATC GCT ATA TGC Met Lys Thr Leu Tyr Ile Ile Ala Ile Cys 1 5 10	53
TCG CTC CTC ATT TCG TTG TGT ACT GGA AGA CCG GAA AAA AAG TGC GGT Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro Glu Lys Lys Cys Gly 15 20 25	101		
CCC GGT GAA AGA CTC GCC TGT GGC AAT AAG AAG CCA TGC GAG CGC AAG Pro Gly Glu Arg Leu Ala Cys Gly Asn Lys Lys Pro Cys Glu Arg Lys 30 35 40	149		
TGC AAA ATA GAG ACA AGT GAG GAG GAG GAT GAC TAC CCA GAG GGA ACC Cys Lys Ile Glu Thr Ser Glu Glu Glu Asp Asp Tyr Pro Glu Gly Thr 45 50 55	197		
GAA CGT TTT CGA TGC CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA TGC Glu Arg Phe Arg Cys Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu Cys 60 65 70	245		
ATA TGC GAT GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT Ile Cys Asp Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr 75 80 85 90	293		
GAT GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA Asp Asp Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro 95 100 105	341		
TAAACCCAAT AATGACCCT GGCTCCATT CTTCGTGACC AGCGTCGGTG GTTGACAGTC	401		
TCCCCCTGCAT CTTAGTAGTT TTGCTTGATA ATGTATCCAT AAACAGTACT TTCTGAGATA	461		
GAATAAAGCT CTCAACT	478		

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 21...335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATTCCGTA CTACTCAACG	ATG AAG ACG CTC TAT ATT ATC GCT ATA TGC	50
	Met Lys Thr Leu Tyr Ile Ile Ala Ile Cys	
	1 5 10	
TCG CTG CTC TTT TCA CTG TGT ACT GGA AGA CCG GAA AAA AAG TGC GGT	Ser Leu Leu Phe Ser Leu Cys Thr Gly Arg Pro Glu Lys Lys Cys Gly	98
	15 20 25	
CCC GGT GAA AGA CTC GAC TGT GCC AAC AAG CCA TGC GAG CCC AAG	Pro Gly Glu Arg Leu Asp Cys Ala Asn Lys Lys Pro Cys Glu Pro Lys	146
	30 35 40	
TGC AAA ATA GAG ACA AGT GAG GAG GAT GAC GAC GTA GAG GAT ACC	Cys Lys Ile Glu Thr Ser Glu Glu Asp Asp Asp Val Glu Asp Thr	194
	45 50 55	
GAT GTG AGA TGC CTC GTA CGT GTG TGT GAA CGT CCT CTT AAA TGC ATA	Asp Val Arg Cys Leu Val Arg Val Cys Glu Arg Pro Leu Lys Cys Ile	242
	60 65 70	
TGC AAG GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT	Cys Lys Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp	290
	75 80 85 90	
GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA TAAACC	Asp Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro	341
	95 100 105	
CAATAATGAC CACTGGCTCC CATTCTTCGT GATCAGCGTC GGTGGTTGAC AGTCTCCCCCT		401
GCATCTTAGT TGCTTGCTT GATAATCTAT ACATAAACAG TACTTTCTGA GATAGAATAA		461
AGCTCTCAAC T		472

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 57...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAATTCCGGA CTTACTAGTA CTCAGCGAAT CAAATACGAC TTACTACTAC TCAACG ATG	59
	Met 1
AAG ACG CTC TCT GCT ATC CCT ATA ATG CTG CTC CTG GTA TCG CAA TGC	107
Lys Thr Leu Ser Ala Ile Pro Ile Met Leu Leu Leu Val Ser Gln Cys	
5 10 15	
AGT GGA AAA TCA CTG TGG GAT CAG AAG TGT GGT GAG AAT GAA AGG CTC	155
Ser Gly Lys Ser Leu Trp Asp Gln Lys Cys Gly Glu Asn Glu Arg Leu	
20 25 30	
GAC TGT GGC AAT CAG AAG GAC TGT GAG CGC AAG TGC GAT GAT AAA AGA	203
Asp Cys Gly Asn Gln Lys Asp Cys Glu Arg Lys Cys Asp Asp Lys Arg	
35 40 45	
AGT GAA GAA GAA ATT ATG CAG GCA TGT CTC ACA CGT CAA TGT CTT CCT	251
Ser Glu Glu Glu Ile Met Gln Ala Cys Leu Thr Arg Gln Cys Leu Pro	
50 55 60 65	
CCT GTT TGC GTA TGT GAA GAT GGA TTC TAC AGA AAT GAC AAC GAC CAA	299
Pro Val Cys Val Cys Glu Asp Gly Phe Tyr Arg Asn Asp Asn Asp Gln	
70 75 80	
TGT GTT GAT GAA GAA GAA TGC AAT ATG GAG TTT ATT ACT TTC GCA CCA TG	349
Cys Val Asp Glu Glu Glu Cys Asn Met Glu Phe Ile Thr Phe Ala Pro	
85 90 95	
AAGCAAATGA CAGCCGATGG TTTGGACTCT CGCTACAGAT CACAGCTTTA CTGTTTCCCT	409
TGCATCATAG TAGTTTGCT AGATAGTGT A TATATTAGCA TGATTTCTG ATAGGGAGAA	469
TAAAGCTTTC CAATTTTC	487

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCCGCG GAATTCCGCA ACG ATG AAG ACG CTC TAT ATT ATC GCT ATA TGC	53
Met Lys Thr Leu Tyr Ile Ile Ala Ile Cys	
1 5 10	

TCG CTC CTC ATT TCG CTG TGT ACT GGA AGA CCG GAA AAA AAG TGC GGT Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro Glu Lys Lys Cys Gly 15 20 25	101
CCC GGT GAA AGA CTC GAC TGT GCC AAC AAG AAG CCA TGC GAG CCC AAG Pro Gly Glu Arg Leu Asp Cys Ala Asn Lys Lys Pro Cys Glu Pro Lys 30 35 40	149
TGC AAA ATA GAG ACA AGT GAG GAG GAT GAC GAC GTA GAG GAA ACC Cys Lys Ile Glu Thr Ser Glu Glu Asp Asp Asp Val Glu Glu Thr 45 50 55	197
GAT GTG AGA TGC CTC GTA CGT GTG TGT GAA CGG CCT CTT AAA TGC ATA Asp Val Arg Cys Leu Val Arg Val Cys Glu Arg Pro Leu Lys Cys Ile 60 65 70	245
TGC AAG GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT Cys Lys Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp 75 80 85 90	293
GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA TAAACC Asp Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro 95 100 105	344
CAATAATGAC CACTGGCTCC CATTCTTCGT GATCAGCGTC GGTGGTTGAC AGTCTCCCCT GCATCTTAGT TGCTTGCTT GATAATCTAT ACATAAACAG TACTTTCTGA GATAGAATAA AGCTCTCAAC TAC	404 464 477

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ancylostoma caninum*

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCCGGA AAA ATG CTG ATG CTC TAC CTT GTT CCT ATC TGG TTG CTA Met Leu Met Leu Tyr Leu Val Pro Ile Trp Leu Leu 1 5 10	49
CTC ATT TCG CAA TGC AGT GGA AAA TCC GCG AAG AAA TGT GGT CTC AAT Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys Lys Cys Gly Leu Asn 15 20 25	97
GAA AAA TTG GAC TGT GGC AAT CTG AAG GCA TGC GAG AAA AAG TGC AGC Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser 30 35 40	145

GAC TTG GAC AAT GAG GAG GAT TAT AAG GAG GAA GAT GAG TCG AAA TGC Asp Leu Asp Asn Glu Glu Asp Tyr Lys Glu Glu Asp Glu Ser Lys Cys 45 50 55 60	193
CGA TCA CGT GAA TGT AGT CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC Arg Ser Arg Glu Cys Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe 65 70 75	241
TAC AGA AAC AAG AAG GGC CAA TGT GTG ACA AGA GAT GAT TGC GAG TAT Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp Asp Cys Glu Tyr 80 85 90	289
GAC AAT ATG GAG ATT ATC ACT TTT CCA CCA GAA GAT AAA TGT GGT CCC Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Lys Cys Gly Pro 95 100 105	337
GAT GAA TGG TTC GAC TGG TGT GGA ACT TAC AAG CAG TGT GAG CGC AAG Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys Gln Cys Glu Arg Lys 110 115 120	385
TGC AAT AAG GAG CTA AGT GAG AAA GAT GAA GAG GCA TGC CTC TCA CGT Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Ala Cys Leu Ser Arg 125 130 135 140	433
GCT TGT ACT GGT CGT GCT TGT GTT TGC AAC GAC GGA CTG TAC AGA GAC Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp 145 150 155	481
GAT TTT GGC AAT TGT GTT GAG AAA GAC GAA TGT AAC GAT ATG GAG ATT Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile 160 165 170	529
ATC ACT TTT CCA CCG GAA ACC AAA CAC TGACCAAAGG CTCTAACTCT CGCTACAT Ile Thr Phe Pro Pro Glu Thr Lys His 175 180	584
AACGTCAGTG CTTGAATTGC CCCTTTACGA GTTAGTAATT TTGACTAACT CTGTGTAATT	644
GAGCATTGTC TACTGATGGT GAAAATGAAG TGTTCAATGT CT	686

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCCGCG GAATTCCGGT TGGCGGCAGA AAA ATG CTG ATG CTC TAC CTT GTT

54

Met Leu Met Leu Tyr Leu Val	
1	5
CCT ATC TGG TTC CTG CTC ATT TCG CAA TGC AGT GGA AAA TCC GCG AAG Pro Ile Trp Phe Leu Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys 10 15 20	102
AAA TGT GGC CTC AAT GAA AAA TTG GAC TGT GGC AAT CTG AAG GCA TGC Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala Cys 25 30 35	150
GAG AAA AAG TGC AGC GAC TTG GAC AAT GAG GAG GAT TAT GGG GAG GAA Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp Tyr Gly Glu Glu 40 45 50 55	198
GAT GAG TCG AAA TGC CGA TCA CGT GAA TGT ATT GGT CGT GTT TGC GTA Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ile Gly Arg Val Cys Val 60 65 70	246
TGC GAT GAA GGA TTC TAC AGA AAC AAG AAG GGC CAA TGT GTG ACA AGA Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg 75 80 85	294
GAC GAT TGC GAG TAT GAC AAT ATG GAG ATT ATC ACT TTT CCA CCA GAA Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu 90 95 100	342
GAT AAA TGT GGT CCC GAT GAA TGG TTC GAC TGG TGT GGA ACT TAC AAG Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys 105 110 115	390
CAG TGT GAG CGC AAG TGC AGT GAG GAG CTA AGT GAG AAA AAT GAG GAG Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser Glu Lys Asn Glu Glu 120 125 130 135	438
GCA TGC CTC TCA CGT GCT TGT ACT GGT CGT GCT TGC GTT TGC AAC GAC Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp 140 145 150	486
GGA TTG TAT AGA GAC GAT TTT GGC AAT TGT GTT GAG AAA GAC GAA TGT Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys 155 160 165	534
AAC GAT ATG GAG ATT ATC ACT TTT CCA CCG GAA ACC AAA CAC TGACCAAAGG Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys His 170 175 180	586
CTCTAGCTCT CGCTACATAA CGTCAGTGCT TGAATTGTCC CTTTACGTGT TAGTAATT GACTAACTCT GTGTATTGTA GCATTGTCTA CTAATGGTGA AAATGAAGCT TTTCAATGAC	646 706
T	707

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 31...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCCGTA CGACCTACTA CTACTCAACG	ATG AAG GCG CTC TAT GTT ATC TCT	54
	Met Lys Ala Leu Tyr Val Ile Ser	
	1	5
ATA ACG TTG CTC CTG GTA TGG CAA TGC AGT GCA AGA ACA GCG AGG AAA		102
Ile Thr Leu Leu Leu Val Trp Gln Cys Ser Ala Arg Thr Ala Arg Lys		
10	15	20
CCC CCA ACG TGT GGT GAA AAT GAA AGG GTC GAA TGG TGT GGC AAG CAG		150
Pro Pro Thr Cys Gly Glu Asn Glu Arg Val Glu Trp Cys Gly Lys Gln		
25	30	35
TGC GAG ATC ACA TGT GAC GAC CCA GAT AAG ATA TGC CGC TCA CTC GCT		198
Cys Glu Ile Thr Cys Asp Asp Pro Asp Lys Ile Cys Arg Ser Leu Ala		
45	50	55
TGT CCT GGT CCT CCT GCT TGC GTA TGC GAC GAC GGA TAC TAC AGA GAC		246
Cys Pro Gly Pro Pro Ala Cys Val Cys Asp Asp Gly Tyr Tyr Arg Asp		
60	65	70
ACG AAC GTT GGC TTG TGT GTA CAA TAT GAC GAA TGC AAC GAT ATG GAT		294
Thr Asn Val Gly Leu Cys Val Gln Tyr Asp Glu Cys Asn Asp Met Asp		
75	80	85
ATT ATT ATG GTT TCA TAGGGTTGAC TGAAGAACATCG AACAAACCGGT GCACAACCTTC		349
Ile Ile Met Val Ser		
90		
TATGCTTGAC TATCTCTCTT GCATCATGCA AGTTAGCTA GATAGTGTAT ATATTAGCAA		409
GACCCCTTGG GGAGAACATGAA GCTTCCCAAC TATATTAAAT CAATAACGTT TTCGCTTCAT		469
GTACACGTGC TCAGCACATT CATATCCACT CCTCACACTC CATGAAAGCA GTGAAATGTT		529

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Necator americanus

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 16...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCCAACTCTT CGAAC ATG ATT CGA GGC CTC GTT CTT TCT CTC CTG TTT	51
Met Ile Arg Gly Leu Val Leu Leu Ser Leu Leu Phe	
1 5 10	
TGC GTC ACT TTT GCA GCG AAG AGA GAT TGT CCA GCA AAT GAG GAA TGG	99
Cys Val Thr Phe Ala Ala Lys Arg Asp Cys Pro Ala Asn Glu Glu Trp	
15 20 25	
AGG GAA TGT GGC ACT CCA TGT GAA CCA AAA TGC AAT CAA CCG ATG CCA	147
Arg Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Gln Pro Met Pro	
30 35 40	
GAT ATA TGT ACT ATG AAT TGT ATC GTC GAT GTG TGT CAA TGC AAG GAG	195
Asp Ile Cys Thr Met Asn Cys Ile Val Asp Val Cys Gln Cys Lys Glu	
45 50 55 60	
GGA TAC AAG CGT CAT GAA ACG AAG GGA TGC TTA AAG GAA GGA TCA GCT	243
Gly Tyr Lys Arg His Glu Thr Lys Gly Cys Leu Lys Glu Gly Ser Ala	
65 70 75	
GAT TGT AAA TAAGTTATCA GAACGCTCGT TTTGTCTTAC ATTAGATGGG TGAGCTGATG	302
Asp Cys Lys	
TATCTGTCAG ATAAACTCTT TCTTCTAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA	361

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp Cys Gly	
1 5 10 15	
Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu Glu Pro Pro Glu Glu	
20 25 30	
Glu Asp Pro Ile Cys Arg Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys	
35 40 45	
Val Cys Lys Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val	
50 55 60	
Arg Glu Glu Glu Cys Asp Gln His Glu Ile Ile His Val	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Lys	Ala	Tyr	Pro	Glu	Cys	Gly	Glu	Asn	Glu	Trp	Leu	Asp	Val	Cys	Gly
1				5					10					15	
Thr	Lys	Lys	Pro	Cys	Glu	Ala	Lys	Cys	Ser	Glu	Glu	Glu	Glu	Glu	Asp
	20						25			30					
Pro	Ile	Cys	Arg	Ser	Phe	Ser	Cys	Pro	Gly	Pro	Ala	Ala	Cys	Val	Cys
	35				40						45				
Glu	Asp	Gly	Phe	Tyr	Arg	Asp	Thr	Val	Ile	Gly	Asp	Cys	Val	Lys	Glu
	50				55				60						
Glu	Glu	Cys	Asp	Gln	His	Glu	Ile	Ile	His	Val					
	65				70			75							

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Arg	Thr	Ala	Arg	Lys	Pro	Pro	Thr	Cys	Gly	Glu	Asn	Glu	Arg	Val	Glu
1				5					10				15		
Trp	Cys	Gly	Lys	Gln	Cys	Glu	Ile	Thr	Cys	Asp	Asp	Pro	Asp	Lys	Ile
	20					25				30					

Cys Arg Ser Leu Ala Cys Pro Gly Pro Pro Ala Cys Val Cys Asp Asp
 35 40 45

Gly Tyr Tyr Arg Asp Thr Asn Val Gly Leu Cys Val Gln Tyr Asp Glu
 50 55 60

Cys Asn Asp Met Asp Ile Ile Met Val Ser
 65 70

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Lys Pro Ser Glu Lys Glu Cys Gly Pro His Glu Arg Leu Asp Cys Gly
 1 5 10 15

Asn Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu Glu
 20 25 30

Glu Asp Asp Tyr Glu Glu Gly Thr Glu Arg Phe Arg Cys Leu Leu Arg
 35 40 45

Val Cys Asp Gln Pro Tyr Glu Cys Ile Cys Asp Asp Gly Tyr Tyr Arg
 50 55 60

Asn Lys Lys Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe
 65 70 75 80

Met Glu Phe Ile Thr Phe Ala Pro
 85

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Arg Pro Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Ala Cys Gly Asn
 1 5 10 15

Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu Glu Glu
 20 25 30
 Asp Asp Tyr Pro Glu Gly Thr Glu Arg Phe Arg Cys Leu Leu Arg Val
 35 40 45
 Cys Asp Gln Pro Tyr Glu Cys Ile Cys Asp Asp Gly Tyr Tyr Arg Asn
 50 55 60
 Lys Lys Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met
 65 70 75 80
 Glu Phe Ile Thr Phe Ala Pro
 85

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Pro Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn
 1 5 10 15
 Lys Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu Glu Glu
 20 25 30
 Asp Asp Asp Val Glu Asp Thr Asp Val Arg Cys Leu Val Arg Val Cys
 35 40 45
 Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp Gly Tyr Tyr Arg Asn Lys
 50 55 60
 Lys Gly Glu Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu
 65 70 75 80
 Phe Ile Thr Phe Ala Pro
 85

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg	Pro	Glu	Lys	Lys	Cys	Gly	Pro	Gly	Glu	Arg	Leu	Asp	Cys	Ala	Asn
1				5				10					15		
Lys	Lys	Pro	Cys	Glu	Pro	Lys	Cys	Lys	Ile	Glu	Thr	Ser	Glu	Glu	Glu
								25					30		
Asp	Asp	Asp	Val	Glu	Glu	Thr	Asp	Val	Arg	Cys	Leu	Val	Arg	Val	Cys
								40				45			
Glu	Arg	Pro	Leu	Lys	Cys	Ile	Cys	Lys	Asp	Gly	Tyr	Tyr	Arg	Asn	Lys
								55			60				
Lys	Gly	Glu	Cys	Val	Thr	Asp	Asp	Val	Cys	Gln	Glu	Asp	Phe	Met	Glu
65					70					75				80	
Phe	Ile	Thr	Phe	Ala	Pro										
					85										

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys	Ser	Leu	Trp	Asp	Gln	Lys	Cys	Gly	Glu	Asn	Glu	Arg	Leu	Asp	Cys
1				5				10				15			
Gly	Asn	Gln	Lys	Asp	Cys	Glu	Arg	Lys	Cys	Asp	Asp	Lys	Arg	Ser	Glu
								25				30			
Glu	Glu	Ile	Met	Gln	Ala	Cys	Leu	Thr	Arg	Gln	Cys	Leu	Pro	Pro	Val
								40			45				
Cys	Val	Cys	Glu	Asp	Gly	Phe	Tyr	Arg	Asn	Asp	Asn	Asp	Gln	Cys	Val
								55			60				
Asp	Glu	Glu	Glu	Cys	Asn	Met	Glu	Phe	Ile	Thr	Phe	Ala	Pro		
					65		70			75					

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Lys	Pro	Asn	Asn	Val	Met	Thr	Asn	Ala	Cys	Gly	Leu	Asn	Glu	Tyr	Phe
1				5					10				15		
Ala	Glu	Cys	Gly	Asn	Met	Lys	Glu	Cys	Glu	His	Arg	Cys	Asn	Glu	Glu
	20					25				30					
Glu	Asn	Glu	Glu	Arg	Asp	Glu	Glu	Arg	Ile	Thr	Ala	Cys	Leu	Ile	Arg
	35				40					45					
Val	Cys	Phe	Arg	Pro	Gly	Ala	Cys	Val	Cys	Lys	Asp	Gly	Phe	Tyr	Arg
	50				55					60					
Asn	Arg	Thr	Gly	Ser	Cys	Val	Glu	Glu	Asp	Asp	Cys	Glu	Tyr	Glu	Asn
	65			70			75						80		
Met	Glu	Phe	Ile	Thr	Phe	Ala	Pro	Glu							
			85												

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	82 amino acids
(B) TYPE:	amino acid
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val	Pro	Ile	Cys	Gly	Ser	Asn	Glu	Arg	Tyr	Ser	Asp	Cys	Gly	Asn	Asp
1				5				10				15			
Lys	Gln	Cys	Glu	Arg	Lys	Cys	Asn	Glu	Asp	Asp	Tyr	Glu	Lys	Gly	Asp
	20				25			25			30				
Glu	Ala	Cys	Arg	Ser	His	Val	Cys	Glu	Arg	Pro	Gly	Ala	Cys	Val	Cys
	35				40			40			45				
Glu	Asp	Gly	Phe	Tyr	Arg	Asn	Lys	Lys	Gly	Ser	Cys	Val	Glu	Ser	Asp
	50				55			55			60				
Asp	Cys	Glu	Tyr	Asp	Asn	Met	Asp	Phe	Ile	Thr	Phe	Ala	Pro	Glu	Thr
	65			70				70		75			80		
Ser	Arg														

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Ancylostoma caninum
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn
 1 5 10 15

Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp
 20 25 30

Tyr Lys Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser Arg
 35 40 45

Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln
 50 55 60

Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr
 65 70 75 80

Phe Pro Pro Glu

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Ancylostoma caninum
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn
 1 5 10 15

Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp
 20 25 30

Tyr Gly Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ile Gly
 35 40 45

Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln
 50 55 60

Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr
 65 70 75 80

Phe Pro Pro Glu

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys	Ala	Ala	Lys	Lys	Cys	Gly	Leu	Asn	Glu	Arg	Leu	Asp	Cys	Gly	Asn
1				5				10					15		
Leu	Lys	Gln	Cys	Glu	Pro	Lys	Cys	Ser	Asp	Leu	Glu	Ser	Glu	Glu	Tyr
				20				25				30			
Glu	Glu	Glu	Asp	Glu	Ser	Lys	Cys	Arg	Ser	Arg	Glu	Cys	Ser	Arg	Arg
				35			40				45				
Val	Cys	Val	Cys	Asp	Glu	Gly	Phe	Tyr	Arg	Asn	Lys	Lys	Gly	Lys	Cys
				50			55				60				
Val	Ala	Lys	Asp	Val	Cys	Glu	Asp	Asp	Asn	Met	Glu	Ile	Ile	Thr	Phe
	65				70				75				80		
Pro	Pro	Glu													

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp	Lys	Cys	Gly	Pro	Asp	Glu	Trp	Phe	Asp	Trp	Cys	Gly	Thr	Tyr	Lys
1				5				10				15			
Gln	Cys	Glu	Arg	Lys	Cys	Asn	Lys	Glu	Leu	Ser	Glu	Lys	Asp	Glu	Glu
				20				25				30			
Ala	Cys	Leu	Ser	Arg	Ala	Cys	Thr	Gly	Arg	Ala	Cys	Val	Cys	Asn	Asp
				35			40				45				
Gly	Leu	Tyr	Arg	Asp	Asp	Phe	Gly	Asn	Cys	Val	Glu	Lys	Asp	Glu	Cys
				50			55				60				
Asn	Asp	Met	Glu	Ile	Ile	Thr	Phe	Pro	Pro	Glu	Thr	Lys	His		

65

70

75

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp	Lys	Cys	Gly	Pro	Asp	Glu	Trp	Phe	Asp	Trp	Cys	Gly	Thr	Tyr	Lys
1					5				10					15	
Gln	Cys	Glu	Arg	Lys	Cys	Ser	Glu	Glu	Leu	Ser	Glu	Lys	Asn	Glu	Glu
						20		25				30			
Ala	Cys	Leu	Ser	Arg	Ala	Cys	Thr	Gly	Arg	Ala	Cys	Val	Cys	Asn	Asp
					35		40				45				
Gly	Leu	Tyr	Arg	Asp	Asp	Phe	Gly	Asn	Cys	Val	Glu	Lys	Asp	Glu	Cys
					50		55			60					
Asn	Asp	Met	Glu	Ile	Ile	Thr	Phe	Pro	Pro	Glu	Thr	Lys	His		
					65		70			75					

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys	Cys	Pro	Thr	Asp	Glu	Trp	Phe	Asp	Trp	Cys	Gly	Thr	Tyr	Lys	His
1					5				10				15		
Cys	Glu	Leu	Lys	Cys	Asp	Arg	Glu	Leu	Thr	Glu	Lys	Glu	Gln	Ala	
					20			25			30				
Cys	Leu	Ser	Arg	Val	Cys	Glu	Lys	Ser	Ala	Cys	Val	Cys	Asn	Asp	Gly
					35		40			45					

Leu Tyr Arg Asp Lys Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn
 50 55 60
 Asp Met Glu Ile Ile Thr Phe Ala Pro Glu Glu Thr Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Asp Glu Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys
 1 5 10 15
 Lys Cys Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Glu
 20 25 30
 Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Lys Asp
 35 40 45
 Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro His Asp Glu Cys
 50 55 60
 Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys His
 65 70 75

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Lys Ala Phe Pro Lys Cys Asp Val Asn Glu Arg Phe Glu Val Cys Gly
 1 5 10 15
 Asn Leu Lys Glu Cys Glu Leu Lys Cys Asp Glu Asp Pro Lys Ile Cys
 20 25 30

Ser Arg Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp Asp Gly Phe
 35 40 45

Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu Asp Glu Cys Asn Asp
 50 55 60

Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma ceylanicum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Arg Thr Val Lys Lys Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly
 1 5 10 15

Asn Ala Lys Asp Cys Glu Thr Lys Cys Gly Glu Glu Lys Val Cys
 20 25 30

Arg Ser Arg Glu Cys Thr Ser Pro Gly Ala Cys Val Cys Glu Gln Gly
 35 40 45

Phe Tyr Arg Asp Pro Ala Gly Asp Cys Val Thr Asp Glu Glu Cys Asp
 50 55 60

Glu Trp Asn Asn Met Glu Ile Ile Thr Met Pro Lys Gln
 65 70 75

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Lys Ala Thr Met Gln Cys Gly Glu Asn Glu Lys Tyr Asp Ser Cys Gly
 1 5 10 15

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Ser Lys Glu Cys Asp Lys Lys Cys Lys Tyr Asp Gly Val Glu Glu Glu
          20           25           30

Asp Asp Glu Glu Pro Asn Val Pro Cys Leu Val Arg Val Cys His Gln
          35           40           45

Asp Cys Val Cys Glu Glu Gly Phe Tyr Arg Asn Lys Asp Asp Lys Cys
          50           55           60

Val Ser Ala Glu Asp Cys Glu Leu Asp Asn Met Asp Phe Ile Tyr Pro
          65           70           75           80

Gly Thr Arg Asn

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(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

ORIGINAL SOURCE:

(A) ORGANISM: *Heligmosomoides*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60.

Lys	Thr	Cys	Gly	Pro	Asn	Glu	Glu	Tyr	Thr	Glu	Cys	Gly	Thr	Pro	Cys
1					5					10					15
Glu	Pro	Lys	Cys	Asn	Glu	Pro	Met	Pro	Asp	Ile	Cys	Thr	Leu	Asn	Cys
							20		25						30
Ile	Val	Asn	Val	Cys	Gln	Cys	Lys	Pro	Gly	Phe	Lys	Arg	Gly	Pro	Lys
							35		40						45
Gly	Cys	Val	Ala	Pro	Gly	Pro	Gly	Cys	Lys						
							50		55						

(2) INFORMATION FOR SEO ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

ORIGINAL SOURCE:
(A) ORGANISM: *Necator americanus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys	Arg	Asp	Cys	Pro	Ala	Asn	Glu	Glu	Trp	Arg	Glu	Cys	Gly	Thr	Pro
1															15
Cys	Glu	Pro	Lys	Cys	Asn	Gln	Pro	Met	Pro	Asp	Ile	Cys	Thr	Met	Asn
								25							30
Cys	Ile	Val	Asp	Val	Cys	Gln	Cys	Lys	Glu	Gly	Tyr	Lys	Arg	His	Glu
								35							45
Thr	Lys	Gly	Cys	Leu	Lys	Glu	Gly	Ser	Ala	Asp	Cys	Lys			
								50							60

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	171 amino acids
(B) TYPE:	amino acid
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM:	Ancylostoma ceylanicum
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys	Pro	Asn	Asn	Val	Met	Thr	Asn	Ala	Cys	Gly	Leu	Asn	Glu	Tyr	Phe
1															15
Ala	Glu	Cys	Gly	Asn	Met	Lys	Glu	Cys	Glu	His	Arg	Cys	Asn	Glu	Glu
								20							30
Glu	Asn	Glu	Glu	Arg	Asp	Glu	Glu	Arg	Ile	Thr	Ala	Cys	Leu	Ile	Arg
								35							45
Val	Cys	Phe	Arg	Pro	Gly	Ala	Cys	Val	Cys	Lys	Asp	Gly	Phe	Tyr	Arg
								50							60
Asn	Arg	Thr	Gly	Ser	Cys	Val	Glu	Glu	Asp	Asp	Cys	Glu	Tyr	Glu	Asn
								65							80
Met	Glu	Phe	Ile	Thr	Phe	Ala	Pro	Glu	Val	Pro	Ile	Cys	Gly	Ser	Asn
								85							95
Glu	Arg	Tyr	Ser	Asp	Cys	Gly	Asn	Asp	Lys	Gln	Cys	Glu	Arg	Lys	Cys
								100							110
Asn	Glu	Asp	Asp	Tyr	Glu	Lys	Gly	Asp	Glu	Ala	Cys	Arg	Ser	His	Val
								115							125
Cys	Glu	Arg	Pro	Gly	Ala	Cys	Val	Cys	Glu	Asp	Gly	Phe	Tyr	Arg	Asn
								130							140
Lys	Lys	Gly	Ser	Cys	Val	Glu	Ser	Asp	Asp	Cys	Glu	Tyr	Asp	Asn	Met
								145							160
Asp	Phe	Ile	Thr	Phe	Ala	Pro	Glu	Thr	Ser	Arg					
								165							170

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys	Ser	Ala	Lys	Lys	Cys	Gly	Leu	Asn	Glu	Lys	Leu	Asp	Cys	Gly	Asn
1				5				10						15	
Leu	Lys	Ala	Cys	Glu	Lys	Lys	Cys	Ser	Asp	Leu	Asp	Asn	Glu	Glu	Asp
				20				25					30		
Tyr	Lys	Glu	Glu	Asp	Glu	Ser	Lys	Cys	Arg	Ser	Arg	Glu	Cys	Ser	Arg
				35			40				45				
Arg	Val	Cys	Val	Cys	Asp	Glu	Gly	Phe	Tyr	Arg	Asn	Lys	Lys	Gly	Gln
				50			55				60				
Cys	Val	Thr	Arg	Asp	Asp	Cys	Glu	Tyr	Asp	Asn	Met	Glu	Ile	Ile	Thr
				65			70				75		80		
Phe	Pro	Pro	Glu	Asp	Lys	Cys	Gly	Pro	Asp	Glu	Trp	Phe	Asp	Trp	Cys
				85			90				95				
Gly	Thr	Tyr	Lys	Gln	Cys	Glu	Arg	Lys	Cys	Asn	Lys	Glu	Leu	Ser	Glu
				100			105				110				
Lys	Asp	Glu	Glu	Ala	Cys	Leu	Ser	Arg	Ala	Cys	Thr	Gly	Arg	Ala	Cys
				115			120				125				
Val	Cys	Asn	Asp	Gly	Leu	Tyr	Arg	Asp	Asp	Phe	Gly	Asn	Cys	Val	Glu
				130			135				140				
Lys	Asp	Glu	Cys	Asn	Asp	Met	Glu	Ile	Ile	Thr	Phe	Pro	Pro	Glu	Thr
				145			150				155		160		
Lys His															

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn
 1 5 10 15

Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp
 20 25 30

Tyr Gly Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ile Gly
 35 40 45

Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Gln
 50 55 60

Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr
 65 70 75 80

Phe Pro Pro Glu Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys
 85 90 95

Gly Thr Tyr Lys Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser Glu
 100 105 110

Lys Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys
 115 120 125

Val Cys Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu
 130 135 140

Lys Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr
 145 150 155 160

Lys His

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma duodenale

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Ala Ala Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn
 1 5 10 15

Leu Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu Tyr
 20 25 30

Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser Arg Arg
 35 40 45

Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Lys Cys
 50 55 60

Val Ala Lys Asp Val Cys Glu Asp Asp Asn Met Glu Ile Ile Thr Phe
 65 70 75 80

Pro Pro Glu Asp Glu Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly
 85 90 95

Asn Tyr Lys Lys Cys Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys
 100 105 110

Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val
 115 120 125

Cys Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro His
 130 135 140

Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys
 145 150 155 160

His

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa at locations 1 and 2 is an amino acid, provided that at least one of Xaa at locations 1 and 2 is Glu or Asp, Xaa in locations 3 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gly Phe Tyr Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Gly Phe Tyr Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Tyr Tyr Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Tyr Tyr Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Leu Tyr Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Glu Ile Ile His Val
1 5

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asp Ile Ile Met Val
1 5

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Phe Ile Thr Phe Ala Pro
1 5

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Glu Ile Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 and 2 is an amino acid, provided that at least one Xaa is Glu or Asp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Xaa Xaa Gly Phe Tyr Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 and 2 is an amino acid, provided that at least one Xaa is Glu or Asp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Xaa Xaa Gly Phe Tyr Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 and 2 is an amino acid, provided that at least one Xaa is Glu or Asp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Xaa Xaa Gly Tyr Tyr Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 and 2 is an amino acid, provided that at least one Xaa is Glu or Asp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Xaa Xaa Gly Tyr Tyr Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 and 2 is an amino

acid, provided that at least one Xaa is Glu or Asp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Xaa Xaa Gly Leu Tyr Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 1 is an amino acid, preferably Leu; Xaa in location 2 is an amino acid; Xaa in location 3 is an amino acid, preferably Arg; Xaa in location 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Xaa Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 4
is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Xaa Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 9 is
an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 9 is
an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TCAGACATGT ATAATCTCAT GTTGG

25

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AAGGCATACC CGGAGTGTGG TG

22

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: "R" stands for A or G; "N" stands for any base; "Y" stands for C or T; and "M" stands for A or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AARCCNTGYG ARMGGAARTG Y

21

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: "W" stands for A or T; "R" stands for A or G; "N" stands for any base; and

"Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TWRWANCCNT CYTTRCANAC RCA

23

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: "R" stands for A or G; "N" stands for inosine; and "Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AARGCNTAYC CNGARTGYGG NGARAAYGAR TGG

33

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTCGCGGC CGCTTTTTT TTTTTTTT

28

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Lys	Ala	Tyr	Pro	Glu	Cys	Gly	Glu	Asn	Glu	Trp	Leu	Asp	Asp	Cys	Gly	Thr
1				5					10					15		

Gln	Lys	Pro
	20	

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CGGAATTCCG

10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TGGCCTAGCG TCAGGAGT

18

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CCTGACGCTA GGCCATGG

18

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGCGGATAAAC AATTTCACAC AGGA

24

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGTTCTCTC CAATTTGTC CTTGGAAATT ATTTAGCTT TGGCTACTTT GCAATCTGTC	60
TTCGCT	66

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CAGCCAGGTA TCTCCACTAC CGTTGGTTCC GCTGCCGAGG GTTCTTGGA CAAGAGG	57
---	----

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CCTATCCCGCG GAATTCAGAT CTGAATGCGG CCGCTCGAGA CTAGTGGATC C	51
---	----

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCTCGCTCTA GAAGCTTCAG ACATGTATAA TCTCATGTTG G	41
---	----

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Lys Ala Tyr Pro Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GACCAGTCTA GACAATGAAG ATGCTTTACG CTATCG

36

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTGGGAGACC TGATACTCTC AAG

23

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Arg Thr Val Arg Lys Ala Tyr Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Arg Thr Val Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATCCGAAGCT TTGCTAACAT ACTGCGTAAT AAG

33

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TATGGGATGG CCGACTTGGC CTCCGCCTGA GCCTCCACCT TTATCCAAT CCAAATAAGA 60

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ATGGGATGGC CGACTTGGCC CTCCGCCTGA GCCTCCACCT TTATCCAAT CCAAATAAGA 60

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TATGGGATGG CCGACTTGGC CGATCCGCC GAGCCTCCAC CTTTATCCA ATCAAATAA 60

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

AGGAGGGGAT CCGCGGCCGC GTGATATGGG ATGGCCGACT TGGCC 45

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGCCAGGGTT TTCCCAAGTCA CGAC

24

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GTTTCGAGTT CCGGGATATA TAAAGTCC

28

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 5 is Arg, Pro or Lys.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Lys Pro Cys Glu Xaa Lys Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 2 is Val, Ile or Gln; Xaa in location 4 is Lys, Asp, Glu or Gln; Xaa in location 5 is Asp or Glu; Xaa in location 7 is Phe or Tyr.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Cys Xaa Cys Xaa Xaa Gly Xaa Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GACCAGTCTA GACCACCATG GCGGTGCTTT ATTCAAGTAGC AATA

44

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCTCGCTCTA GATTATCGTG AGGTTTCTGG TGCAAAAGTG

40

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGCAACGA TGCAGTGTGG TGAG

24

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCTCGCTCTA GAAGCTTCAG TTTCGAGTTC CGGGATATAT AAAGTCC

47

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAGACTTTA AATCACTGTG GGATCAGAAG

30

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

TTCAGGACTA GTTCATGGTG CGAAAGTAAT AAA

33

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GCGTTAAAG CAACGATGCA GTGTGGTG

28

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CGCTCTAGAA GCTTCATGGG TTTCGAGTTC CGGGATATAT AAAGTC

46

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Ancylostoma caninum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Leu	Val	Ser	Tyr	Cys	Ser	Gly	Lys	Ala	Thr	Met	Gln	Cys	Gly	Glu	Asn
1				5						10				15	

Glu	Lys	Tyr	Asp	Ser	Cys	Gly	Ser	Lys	Glu	Cys	Asp	Lys	Lys	Cys	Lys
			20				25					30			

Tyr	Asp	Gly	Val	Glu	Glu	Asp	Asp	Glu	Glu	Pro	Asn	Val	Pro	Cys
	35				40					45				

Leu	Val	Arg	Val	Cys	His	Gln	Asp	Cys	Val	Cys	Glu	Gly	Phe	Tyr
		50				55				60				

Arg	Asn	Lys	Asp	Asp	Lys	Cys	Val	Ser	Ala	Glu	Asp	Cys	Glu	Leu	Asp
65				70					75					80	

Asn	Met	Asp	Phe	Ile	Tyr	Pro	Gly	Thr	Arg	Asn
			85					90		

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 8
is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Cys	Xaa						
1				5			

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6
is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Cys Xaa Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5
is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Cys Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4
is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Cys Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 and 3
is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Cys Xaa Xaa Cys
1

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5
to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Cys Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Cys Xaa Xaa Xaa
 1

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Cys Xaa Cys Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Cys Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Cys Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Cys Xaa Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Cys Xaa Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Cys Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Cys Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Cys Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Cys Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 26 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Cys Xaa
1 5 10 15
Xaa
20 25

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 25 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Cys Xaa
1 5 10 15
Xaa
20 25

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 24 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Cys Xaa
1 5 10 15
Xaa
20

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: . 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Cys	Xaa												
1													15
Xaa Xaa Xaa Xaa													
20													

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Cys	Xaa												
1													15
Xaa Xaa Xaa													

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Cys	Xaa												
1													15
Xaa Xaa													

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Cys Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 12 is an

amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Cys Xaa Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

SBQ-1 LENGTH: 6 amino acids
(A) TYPE: amino acid
(B) TOPOLOGY: linear
(D)

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Cys Xaa Xaa Xaa Xaa Cys
 1 5

(2) INFORMATION FOR SEQ ID NO: 208:

(ii) SEQUENCE CHARACTERISTICS:

SEQUENCE CHARGE: 5 amino acids
(A) LENGTH: amino acid
(B) TYPE: linear
(D) TOPOLOGY:

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

FEATURE: (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Cys Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 209:

(ii) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

FEATURE:
(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 23 is an amino acid.

DESCRIPTION: SEQ ID NO: 209:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:
Xaa Xaa Xaa Cys Xaa Xaa

1

5

10

15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Xaa Xaa Xaa Cys Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

Xaa Xaa Xaa Cys Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
5 10 15
1
Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	19 amino acids
(B)	TYPE:	amino acid
(D)	TOPOLOGY:	linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
5 10 15
1
Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	18 amino acids
(B)	TYPE:	amino acid
(D)	TOPOLOGY:	linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
5 10 15
1

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

Xaa Xaa Xaa Cys Xaa
 1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Xaa Xaa Xaa Cys Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Xaa Xaa Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Cys Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Cys Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 26 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 25 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 24 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Cys Xaa
 1 5 10 15
 Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	22 amino acids
(B)	TYPE:	amino acid
(D)	TOPOLOGY:	linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Cys Xaa
 1 5 10 15
 Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	21 amino acids
(B)	TYPE:	amino acid
(D)	TOPOLOGY:	linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Cys Xaa
 1 5 10 15 20

1

5

10

15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 18 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Cys Xaa
1 5 10 15
Xaa Xaa

- (2) INFORMATION FOR SEQ ID NO: 242:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear - (v) FRAGMENT TYPE: internal fragment
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 17 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Cys Xaa
1 5 10 15
Xaa

- (2) INFORMATION FOR SEQ ID NO: 243:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear - (v) FRAGMENT TYPE: internal fragment
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 16 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Cys Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Cys Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Cys Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 13 is an

108

amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Cys Xaa Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Cys Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Xaa Xaa Xaa Cys Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Xaa Xaa Xaa Cys Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 13 is an amino acid.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 12 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 11 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

Cys Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

Cys Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 26 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 25 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 24 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Cys Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 17 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

Cys Xaa
1 5 10 15

Xaa

- (2) INFORMATION FOR SEQ ID NO: 293:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 16 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Cys Xaa
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 294:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in locations 2 to 15 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Cys Xaa
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an

amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 2 and 3 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Cys Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in location 2 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Cys Xaa
1

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Cys Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

Cys Xaa Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Cys Xaa Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:
Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment
(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Xaa Xaa Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 13 is an amino

acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5						10

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Cys	Xaa	Xaa	Xaa	Xaa
1			5	

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Cys	Xaa	Xaa	Xaa
1			

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 5 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Cys Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 4 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Cys Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Cys Xaa Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in location 2 and locations 4 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Cys Xaa Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Cys Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 26 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Cys	Xaa												
1													15
Xaa													
												20	25

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 25 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Cys	Xaa												
1													15
Xaa													
												20	25

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 24 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Cys	Xaa												
1													15
Xaa													

20

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 23 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Cys Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 22 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Cys Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 21 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 20 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 19 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Cys Xaa
1 5 10 15

Xaa Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 18 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Cys Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 17 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Cys Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 16 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 15 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Cys Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in locations 2 to 14 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 13 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 12 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Cys Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 11 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 10 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 9 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in locations 2 to 8 is an amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
- (D) OTHER INFORMATION: Xaa in locations 2 to 7 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Cys Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE:
- (D) OTHER INFORMATION: Xaa in locations 2 to 6 is an amino acid.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Cys Xaa Xaa Xaa Xaa Xaa
1 5